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SEQIDNO1.ST25
SEQUENCE LISTING

<110> AS-Faktor AB

<120> Novel use

<130> 21016008

<150> GB 0322645.3

<151> 2003-09-26

<160> 2

<170> PatentIn version 3.1

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atg cgg aat gga gac ttc tta ccc acc agg ctg cag gcc cag cag gat 155
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Ala	Val	Asn	Ile	Val	Cys	His	Ser	Lys	Thr	Arg	Ser	Asn	Pro	Glu	Asn
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Asn	Val	Gly	Leu	Ile	Thr	Leu	Ala	Asn	Asp	Cys	Glu	Val	Leu	Thr	Thr
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Leu	Thr	Pro	Asp	Thr	Gly	Arg	Ile	Leu	Ser	Lys	Leu	His	Thr	Val	Gln
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Pro	Lys	Gly	Lys	Ile	Thr	Phe	Cys	Thr	Gly	Ile	Arg	Val	Ala	His	Leu
80					85				90						95
gct	ctg	aag	cac	cga	caa	ggc	aag	aat	cac	aag	atg	cgc	atc	att	gcc
Ala	Leu	Lys	His	Arg	Gln	Gly	Lys	Asn	His	Lys	Met	Arg	Ile	Ile	Ala
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ttt	gtg	gga	agc	cca	gtg	gag	gac	aat	gag	aag	gat	ctg	gtg	aaa	ctg
Phe	Val	Gly	Ser	Pro	Val	Glu	Asp	Asn	Glu	Lys	Asp	Leu	Val	Lys	Leu
			115					120					125		
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Gly	Glu	Glu	Glu	Val	Asn	Thr	Glu	Lys	Leu	Thr	Ala	Phe	Val	Asn	Thr
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ggg	ccc	agt	ttg	gct	gat	gct	ctc	atc	agt	tct	ccg	att	ttg	gct	ggt
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				180					185					190	
gaa	ggt	ggt	gcc	atg	ctg	ggt	ctt	ggt	gcc	agt	gac	ttt	gaa	ttt	gga
Glu	Gly	Gly	Ala	Met	Leu	Gly	Leu	Gly	Ala	Ser	Asp	Phe	Glu	Phe	Gly
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Ala	Ser	Ala	Ala	Glu	Ala	Gly	Ile	Ala	Thr	Thr	Gly	Thr	Glu	Asp	Ser
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gac	gat	gcc	ctg	ctg	aag	atg	acc	atc	agc	cag	caa	gag	ttt	ggc	cgc
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act	ggg	ctt	cct	gac	cta	agc	agt	agt	act	gag	gaa	gag	gag	att	gct
Thr	Gly	Leu	Pro	Asp	Leu	Ser	Ser	Ser	Thr	Glu	Glu	Glu	Glu	Ile	Ala
			275					280					285		
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 Ser Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala
 305 310 315

aag gag gag gat gat tac gac gtg atg cag gac ccc gag ttc ctt cag 1067
 Lys Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln
 320 325 330 335

agt gtc cta gag aac ctc cca ggt gtg gat ccc aac aat gaa gcc att 1115
 Ser Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile
 340 345 350

cga aat gct atg ggc tcc ctg cct ccc agg cca cca agg acg gca aga 1163
 Arg Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg
 355 360 365

agg aca aga agg agg aag aca aga agt gag act gga ggg aaa ggg 1208
 Arg Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
 370 375 380

tagctgagtc tgcttagggg actgggaagc acggaatata gggtagatg tggttatctg 1268

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 35 40 45

Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu
 50 55 60

Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro
 65 70 75 80

Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala
 85 90 95

Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe
 100 105 110

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 115 120 125

Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
 130 135 140

Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
 145 150 155 160

Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro Gly
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Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly Glu
 180 185 190

Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly Val
 195 200 205

Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser Met
 210 215 220

Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg Ala
 225 230 235 240

Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser Asp
 245 250 255

Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg Thr
 260 265 270

Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala Tyr
 275 280 285

Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu Ser
 290 295 300

Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala Lys
 305 310 315 320

Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln Ser
 325 330 335

Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile Arg
 340 345 350

Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg Arg
 355 360 365

Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
 370 375 380